

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: HU, JING-SHAN  
ROSEN, CRAIG A.  
CAO, LIANG

(ii) TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2

(iii) NUMBER OF SEQUENCES: 35

(iv) CORRESPONDENCE ADDRESS:

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(C) CITY: WASHINGTON  
(D) STATE: DC  
(E) COUNTRY: USA  
(F) ZIP: 20005

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: TO BE ASSIGNED  
(B) FILING DATE: HERewith  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/207,550  
(B) FILING DATE: 8-MAR-1994  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/465,968  
(B) FILING DATE: 06-JUN-1995  
(C) CLASSIFICATION:

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: TO BE ASSIGNED  
(B) FILING DATE: 24-DEC-1997  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

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(C) REFERENCE/DOCKET NUMBER: 1488.1000003/EKS

(ix) TELECOMMUNICATION INFORMATION:

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099334 00401  
104220 92455660

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1674 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:  
 (A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 12..80

- (ix) FEATURE:  
 (A) NAME/KEY: mat\_peptide  
 (B) LOCATION: 81..1268

- (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 12..1268

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTCCTTCCAC C ATG CAC TCG CTG GGC TTC TTC TCT GTG GCG TGT TCT CTG	50
Met His Ser Leu Gly Phe Phe Ser Val Ala Cys Ser Leu	
-23 -20 -15	
CTC GCC GCT GCG CTG CTC CCG GGT CCT CGC GAG GCG CCC GCC GCC GCC	98
Leu Ala Ala Ala Leu Leu Pro Gly Pro Arg Glu Ala Pro Ala Ala Ala	
-10 -5 1 5	
GCC GCC TTC GAG TCC GGA CTC GAC CTC TCG GAC GCG GAG CCC GAC GCG	146
Ala Ala Phe Glu Ser Gly Leu Asp Leu Ser Asp Ala Glu Pro Asp Ala	
10 15 20	
GGC GAG GCC ACG GCT TAT GCA AGC AAA GAT CTG GAG GAG CAG TTA CGG	194
Gly Glu Ala Thr Ala Tyr Ala Ser Lys Asp Leu Glu Glu Gln Leu Arg	
25 30 35	
TCT GTG TCC AGT GTA GAT GAA CTC ATG ACT GTA CTC TAC CCA GAA TAT	242
Ser Val Ser Ser Val Asp Glu Leu Met Thr Val Leu Tyr Pro Glu Tyr	
40 45 50	
TGG AAA ATG TAC AAG TGT CAG CTA AGG AAA GGA GGC TGG CAA CAT AAC	290
Trp Lys Met Tyr Lys Cys Gln Leu Arg Lys Gly Gly Trp Gln His Asn	
55 60 65 70	
AGA GAA CAG GCC AAC CTC AAC TCA AGG ACA GAA GAG ACT ATA AAA TTT	338
Arg Glu Gln Ala Asn Leu Asn Ser Arg Thr Glu Glu Thr Ile Lys Phe	
75 80 85	

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GCT GCA GCA CAT TAT AAT ACA GAG ATC TTG AAA AGT ATT GAT AAT GAG Ala Ala Ala His Tyr Asn Thr Glu Ile Leu Lys Ser Ile Asp Asn Glu 90 95 100	386
TGG AGA AAG ACT CAA TGC ATG CCA CGG GAG GTG TGT ATA GAT GTG GGG Trp Arg Lys Thr Gln Cys Met Pro Arg Glu Val Cys Ile Asp Val Gly 105 110 115	434
AAG GAG TTT GGA GTC GCG ACA AAC ACC TTC TTT AAA CCT CCA TGT GTG Lys Glu Phe Gly Val Ala Thr Asn Thr Phe Phe Lys Pro Pro Cys Val 120 125 130	482
TCC GTC TAC AGA TGT GGG GGT TGC TGC AAT AGT GAG GGG CTG CAG TGC Ser Val Tyr Arg Cys Gly Gly Cys Cys Asn Ser Glu Gly Leu Gln Cys 135 140 145 150	530
ATG AAC ACC AGC ACG AGC TAC CTC AGC AAG ACG TTA TTT GAA ATT ACA Met Asn Thr Ser Thr Ser Tyr Leu Ser Lys Thr Leu Phe Glu Ile Thr 155 160 165	578
GTG CCT CTC TCT CAA GGC CCC AAA CCA GTA ACA ATC AGT TTT GCC AAT Val Pro Leu Ser Gln Gly Pro Lys Pro Val Thr Ile Ser Phe Ala Asn 170 175 180	626
CAC ACT TCC TGC CGA TGC ATG TCT AAA CTG GAT GTT TAC AGA CAA GTT His Thr Ser Cys Arg Cys Met Ser Lys Leu Asp Val Tyr Arg Gln Val 185 190 195	674
CAT TCC ATT ATT AGA CGT TCC CTG CCA GCA ACA CTA CCA CAG TGT CAG His Ser Ile Ile Arg Arg Ser Leu Pro Ala Thr Leu Pro Gln Cys Gln 200 205 210	722
GCA GCG AAC AAG ACC TGC CCC ACC AAT TAC ATG TGG AAT AAT CAC ATC Ala Ala Asn Lys Thr Cys Pro Thr Asn Tyr Met Trp Asn Asn His Ile 215 220 225 230	770
TGC AGA TGC CTG GCT CAG GAA GAT TTT ATG TTT TCC TCG GAT GCT GGA Cys Arg Cys Leu Ala Gln Glu Asp Phe Met Phe Ser Ser Asp Ala Gly 235 240 245	818
GAT GAC TCA ACA GAT GGA TTC CAT GAC ATC TGT GGA CCA AAC AAG GAG Asp Asp Ser Thr Asp Gly Phe His Asp Ile Cys Gly Pro Asn Lys Glu 250 255 260	866
CTG GAT GAA GAG ACC TGT CAG TGT GTC TGC AGA GCG GGG CTT CGG CCT Leu Asp Glu Glu Thr Cys Gln Cys Val Cys Arg Ala Gly Leu Arg Pro 265 270 275	914
GCC AGC TGT GGA CCC CAC AAA GAA CTA GAC AGA AAC TCA TGC CAG TGT Ala Ser Cys Gly Pro His Lys Glu Leu Asp Arg Asn Ser Cys Gln Cys 280 285 290	962
GTC TGT AAA AAC AAA CTC TTC CCC AGC CAA TGT GGG GCC AAC CGA GAA Val Cys Lys Asn Lys Leu Phe Pro Ser Gln Cys Gly Ala Asn Arg Glu 295 300 305 310	1010

093326-082401

TTT GAT GAA AAC ACA TGC CAG TGT GTA TGT AAA AGA ACC TGC CCC AGA	1058
Phe Asp Glu Asn Thr Cys Gln Cys Val Cys Lys Arg Thr Cys Pro Arg	
315 320 325	
AAT CAA CCC CTA AAT CCT GGA AAA TGT GCC TGT GAA TGT ACA GAA AGT	1106
Asn Gln Pro Leu Asn Pro Gly Lys Cys Ala Cys Glu Cys Thr Glu Ser	
330 335 340	
CCA CAG AAA TGC TTG TTA AAA GGA AAG AAG TTC CAC CAC CAA ACA TGC	1154
Pro Gln Lys Cys Leu Leu Lys Gly Lys Lys Phe His His Gln Thr Cys	
345 350 355	
AGC TGT TAC AGA CGG CCA TGT ACG AAC CGC CAG AAG GCT TGT GAG CCA	1202
Ser Cys Tyr Arg Arg Pro Cys Thr Asn Arg Gln Lys Ala Cys Glu Pro	
360 365 370	
GGA TTT TCA TAT AGT GAA GAA GTG TGT CGT TGT GTC CCT TCA TAT TGG	1250
Gly Phe Ser Tyr Ser Glu Glu Val Cys Arg Cys Val Pro Ser Tyr Trp	
375 380 385 390	
CAA AGA CCA CAA ATG AGC TAAGATTGTA CTGTTTTCCA GTTCATCGAT	1298
Gln Arg Pro Gln Met Ser	
395	
TTTCTATTAT GGAAACTGT GTTGCCACAG TAGAACTGTC TGTGAACAGA GAGACCCTTG	1358
TGGGTCCATG CTAACAAAGA CAAAAGTCTG TCTTTCCTGA ACCATGTGGA TAACTTTACA	1418
GAAATGGACT GGAGCTCATC TGCAAAGGC CTCTTGTAAG GACTGGTTTT CTGCCAATGA	1478
CCAAACAGCC AAGATTTTCC TCTTGTGATT TCTTTAAAAG AATGACTATA TAATTTATTT	1538
CCACTAAAAA TATTGTTTCT GCATTCATTT TTATAGCAAC AACAATTGGT AAAACTCACT	1598
GTGATCAATA TTTTATATC ATGCAAAATA TGTTTAAAT AAAATGAAAA TTGTATTTAT	1658
AAAAAAAAA AAAAAA	1674

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 419 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met His Ser Leu Gly Phe Phe Ser Val Ala Cys Ser Leu Leu Ala Ala	
-23 -20 -15 -10	
Ala Leu Leu Pro Gly Pro Arg Glu Ala Pro Ala Ala Ala Ala Phe	
-5 1 5	

Glu	Ser	Gly	Leu	Asp	Leu	Ser	Asp	Ala	Glu	Pro	Asp	Ala	Gly	Glu	Ala	10	15	20	25
Thr	Ala	Tyr	Ala	Ser	Lys	Asp	Leu	Glu	Glu	Gln	Leu	Arg	Ser	Val	Ser	30	35	40	
Ser	Val	Asp	Glu	Leu	Met	Thr	Val	Leu	Tyr	Pro	Glu	Tyr	Trp	Lys	Met	45	50	55	
Tyr	Lys	Cys	Gln	Leu	Arg	Lys	Gly	Gly	Trp	Gln	His	Asn	Arg	Glu	Gln	60	65	70	
Ala	Asn	Leu	Asn	Ser	Arg	Thr	Glu	Glu	Thr	Ile	Lys	Phe	Ala	Ala	Ala	75	80	85	
His	Tyr	Asn	Thr	Glu	Ile	Leu	Lys	Ser	Ile	Asp	Asn	Glu	Trp	Arg	Lys	90	95	100	105
Thr	Gln	Cys	Met	Pro	Arg	Glu	Val	Cys	Ile	Asp	Val	Gly	Lys	Glu	Phe	110	115	120	
Gly	Val	Ala	Thr	Asn	Thr	Phe	Phe	Lys	Pro	Pro	Cys	Val	Ser	Val	Tyr	125	130	135	
Arg	Cys	Gly	Gly	Cys	Cys	Asn	Ser	Glu	Gly	Leu	Gln	Cys	Met	Asn	Thr	140	145	150	
Ser	Thr	Ser	Tyr	Leu	Ser	Lys	Thr	Leu	Phe	Glu	Ile	Thr	Val	Pro	Leu	155	160	165	
Ser	Gln	Gly	Pro	Lys	Pro	Val	Thr	Ile	Ser	Phe	Ala	Asn	His	Thr	Ser	170	175	180	185
Cys	Arg	Cys	Met	Ser	Lys	Leu	Asp	Val	Tyr	Arg	Gln	Val	His	Ser	Ile	190	195	200	
Ile	Arg	Arg	Ser	Leu	Pro	Ala	Thr	Leu	Pro	Gln	Cys	Gln	Ala	Ala	Asn	205	210	215	
Lys	Thr	Cys	Pro	Thr	Asn	Tyr	Met	Trp	Asn	Asn	His	Ile	Cys	Arg	Cys	220	225	230	
Leu	Ala	Gln	Glu	Asp	Phe	Met	Phe	Ser	Ser	Asp	Ala	Gly	Asp	Asp	Ser	235	240	245	
Thr	Asp	Gly	Phe	His	Asp	Ile	Cys	Gly	Pro	Asn	Lys	Glu	Leu	Asp	Glu	250	255	260	265
Glu	Thr	Cys	Gln	Cys	Val	Cys	Arg	Ala	Gly	Leu	Arg	Pro	Ala	Ser	Cys	270	275	280	
Gly	Pro	His	Lys	Glu	Leu	Asp	Arg	Asn	Ser	Cys	Gln	Cys	Val	Cys	Lys	285	290	295	
Asn	Lys	Leu	Phe	Pro	Ser	Gln	Cys	Gly	Ala	Asn	Arg	Glu	Phe	Asp	Glu				

300	305	310
Asn Thr Cys Gln Cys Val Cys Lys Arg Thr Cys Pro Arg Asn Gln Pro		
315	320	325
Leu Asn Pro Gly Lys Cys Ala Cys Glu Cys Thr Glu Ser Pro Gln Lys		
330	335	340 345
Cys Leu Leu Lys Gly Lys Lys Phe His His Gln Thr Cys Ser Cys Tyr		
	350 355	360
Arg Arg Pro Cys Thr Asn Arg Gln Lys Ala Cys Glu Pro Gly Phe Ser		
	365 370	375
Tyr Ser Glu Glu Val Cys Arg Cys Val Pro Ser Tyr Trp Gln Arg Pro		
	380 385	390
Gln Met Ser		
395		

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1526 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
- (A) NAME/KEY: sig\_peptide
  - (B) LOCATION: 71..142

- (ix) FEATURE:
- (A) NAME/KEY: mat\_peptide
  - (B) LOCATION: 143..1120

- (ix) FEATURE:
- (A) NAME/KEY: CDS
  - (B) LOCATION: 71..1120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CGAGGCCACG GCTTATGCAA GCAAAGATCT GGAGGAGCAG TTACGGTCTG TGTCCAGTGT	60
AGATGAAGTC ATG ACT GTA CTC TAC CCA GAA TAT TGG AAA ATG TAC AAG	109
Met Thr Val Leu Tyr Pro Glu Tyr Trp Lys Met Tyr Lys	
-24 -20 -15	
TGT CAG CTA AGG AAA GGA GGC TGG CAA CAT AAC AGA GAA CAG GCC AAC	157
Cys Gln Leu Arg Lys Gly Gly Trp Gln His Asn Arg Glu Gln Ala Asn	
-10 -5 1 5	

093576-082401

CTC AAC TCA AGG ACA GAA GAG ACT ATA AAA TTT GCT GCA GCA CAT TAT	205
Leu Asn Ser Arg Thr Glu Glu Thr Ile Lys Phe Ala Ala Ala His Tyr	
10 15 20	
AAT ACA GAG ATC TTG AAA AGT ATT GAT AAT GAG TGG AGA AAG ACT CAA	253
Asn Thr Glu Ile Leu Lys Ser Ile Asp Asn Glu Trp Arg Lys Thr Gln	
25 30 35	
TGC ATG CCA CGG GAG GTG TGT ATA GAT GTG GGG AAG GAG TTT GGA GTC	301
Cys Met Pro Arg Glu Val Cys Ile Asp Val Gly Lys Glu Phe Gly Val	
40 45 50	
GCG ACA AAC ACC TTC TTT AAA CCT CCA TGT GTG TCC GTC TAC AGA TGT	349
Ala Thr Asn Thr Phe Phe Lys Pro Pro Cys Val Ser Val Tyr Arg Cys	
55 60 65	
GGG GGT TGC TGC AAT AGT GAG GGG CTG CAG TGC ATG AAC ACC AGC ACG	397
Gly Gly Cys Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Thr Ser Thr	
70 75 80 85	
AGC TAC CTC AGC AAG ACG TTA TTT GAA ATT ACA GTG CCT CTC TCT CAA	445
Ser Tyr Leu Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu Ser Gln	
90 95 100	
GGC CCC AAA CCA GTA ACA ATC AGT TTT GCC AAT CAC ACT TCC TGC CGA	493
Gly Pro Lys Pro Val Thr Ile Ser Phe Ala Asn His Thr Ser Cys Arg	
105 110 115	
TGC ATG TCT AAA CTG GAT GTT TAC AGA CAA GTT CAT TCC ATT ATT AGA	541
Cys Met Ser Lys Leu Asp Val Tyr Arg Gln Val His Ser Ile Ile Arg	
120 125 130	
CGT TCC CTG CCA GCA ACA CTA CCA CAG TGT CAG GCA GCG AAC AAG ACC	589
Arg Ser Leu Pro Ala Thr Leu Pro Gln Cys Gln Ala Ala Asn Lys Thr	
135 140 145	
TGC CCC ACC AAT TAC ATG TGG AAT AAT CAC ATC TGC AGA TGC CTG GCT	637
Cys Pro Thr Asn Tyr Met Trp Asn Asn His Ile Cys Arg Cys Leu Ala	
150 155 160 165	
CAG GAA GAT TTT ATG TTT TCC TCG GAT GCT GGA GAT GAC TCA ACA GAT	685
Gln Glu Asp Phe Met Phe Ser Ser Asp Ala Gly Asp Asp Ser Thr Asp	
170 175 180	
GGA TTC CAT GAC ATC TGT GGA CCA AAC AAG GAG CTG GAT GAA GAG ACC	733
Gly Phe His Asp Ile Cys Gly Pro Asn Lys Glu Leu Asp Glu Glu Thr	
185 190 195	
TGT CAG TGT GTC TGC AGA GCG GGG CTT CGG CCT GCC AGC TGT GGA CCC	781
Cys Gln Cys Val Cys Arg Ala Gly Leu Arg Pro Ala Ser Cys Gly Pro	
200 205 210	
CAC AAA GAA CTA GAC AGA AAC TCA TGC CAG TGT GTC TGT AAA AAC AAA	829
His Lys Glu Leu Asp Arg Asn Ser Cys Gln Cys Val Cys Lys Asn Lys	
215 220 225	

09635726-082491

CTC TTC CCC AGC CAA TGT GGG GCC AAC CGA GAA TTT GAT GAA AAC ACA	877
Leu Phe Pro Ser Gln Cys Gly Ala Asn Arg Glu Phe Asp Glu Asn Thr	
230 235 240 245	
TGC CAG TGT GTA TGT AAA AGA ACC TGC CCC AGA AAT CAA CCC CTA AAT	925
Cys Gln Cys Val Cys Lys Arg Thr Cys Pro Arg Asn Gln Pro Leu Asn	
250 255 260	
CCT GGA AAA TGT GCC TGT GAA TGT ACA GAA AGT CCA CAG AAA TGC TTG	973
Pro Gly Lys Cys Ala Cys Glu Cys Thr Glu Ser Pro Gln Lys Cys Leu	
265 270 275	
TTA AAA GGA AAG AAG TTC CAC CAC CAA ACA TGC AGC TGT TAC AGA CGG	1021
Leu Lys Gly Lys Lys Phe His His Gln Thr Cys Ser Cys Tyr Arg Arg	
280 285 290	
CCA TGT ACG AAC CGC CAG AAG GCT TGT GAG CCA GGA TTT TCA TAT AGT	1069
Pro Cys Thr Asn Arg Gln Lys Ala Cys Glu Pro Gly Phe Ser Tyr Ser	
295 300 305	
GAA GAA GTG TGT CGT TGT GTC CCT TCA TAT TGG CAA AGA CCA CAA ATG	1117
Glu Glu Val Cys Arg Cys Val Pro Ser Tyr Trp Gln Arg Pro Gln Met	
310 315 320 325	
AGC TAAGATTGTA CTGTTTTCCTA GTTCATCGAT TTTCTATTAT GGAAACTGT	1170
Ser	
GTTGCCACAG TAGAACTGTC TGTGAACAGA GAGACCCTTG TGGGTCCATG CTAACAAAGA	1230
CAAAAGTCTG TCTTTCCTGA ACCATGTGGA TAACTTTACA GAAATGGACT GGAGCTCATC	1290
TGCAAAAGGC CTCTTGTAAG GACTGGTTTT CTGCCAATGA CCAAACAGCC AAGATTTTCC	1350
TCTTGTGATT TCTTTAAAAG AATGACTATA TAATTTATTT CCACTAAAAA TATTGTTTCT	1410
GCATTCATTT TTATAGCAAC AACAATTGGT AAAACTCACT GTGATCAATA TTTTATATC	1470
ATGCAAAATA TGTTTAAAT AAAATGAAAA TTGTATTTAT AAAAAAAAAA AAAAAA	1526

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Thr Val Leu Tyr Pro Glu Tyr Trp Lys Met Tyr Lys Cys Gln Leu
-24 -20 -15 -10

09935726-082401



Arg Lys Gly Gly Trp Gln His Asn Arg Glu Gln Ala Asn Leu Asn Ser  
-5 1 5

Arg Thr Glu Glu Thr Ile Lys Phe Ala Ala Ala His Tyr Asn Thr Glu  
10 15 20

Ile Leu Lys Ser Ile Asp Asn Glu Trp Arg Lys Thr Gln Cys Met Pro  
25 30 35 40

Arg Glu Val Cys Ile Asp Val Gly Lys Glu Phe Gly Val Ala Thr Asn  
45 50 55

Thr Phe Phe Lys Pro Pro Cys Val Ser Val Tyr Arg Cys Gly Gly Cys  
60 65 70

Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Thr Ser Thr Ser Tyr Leu  
75 80 85

Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu Ser Gln Gly Pro Lys  
90 95 100

Pro Val Thr Ile Ser Phe Ala Asn His Thr Ser Cys Arg Cys Met Ser  
105 110 115 120

Lys Leu Asp Val Tyr Arg Gln Val His Ser Ile Ile Arg Arg Ser Leu  
125 130 135

Pro Ala Thr Leu Pro Gln Cys Gln Ala Ala Asn Lys Thr Cys Pro Thr  
140 145 150

Asn Tyr Met Trp Asn Asn His Ile Cys Arg Cys Leu Ala Gln Glu Asp  
155 160 165

Phe Met Phe Ser Ser Asp Ala Gly Asp Asp Ser Thr Asp Gly Phe His  
170 175 180

Asp Ile Cys Gly Pro Asn Lys Glu Leu Asp Glu Glu Thr Cys Gln Cys  
185 190 195 200

Val Cys Arg Ala Gly Leu Arg Pro Ala Ser Cys Gly Pro His Lys Glu  
205 210 215

Leu Asp Arg Asn Ser Cys Gln Cys Val Cys Lys Asn Lys Leu Phe Pro  
220 225 230

Ser Gln Cys Gly Ala Asn Arg Glu Phe Asp Glu Asn Thr Cys Gln Cys  
235 240 245

Val Cys Lys Arg Thr Cys Pro Arg Asn Gln Pro Leu Asn Pro Gly Lys  
250 255 260

Cys Ala Cys Glu Cys Thr Glu Ser Pro Gln Lys Cys Leu Leu Lys Gly  
265 270 275 280

Lys Lys Phe His His Gln Thr Cys Ser Cys Tyr Arg Arg Pro Cys Thr

090300" 020500

285 290 295  
 Asn Arg Gln Lys Ala Cys Glu Pro Gly Phe Ser Tyr Ser Glu Glu Val  
 300 305 310

Cys Arg Cys Val Pro Ser Tyr Trp Gln Arg Pro Gln Met Ser  
 315 320 325

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Arg Thr Leu Ala Cys Leu Leu Leu Leu Gly Cys Gly Tyr Leu Ala  
 1 5 10 15  
 His Val Leu Ala Glu Glu Ala Glu Ile Pro Arg Glu Val Ile Glu Arg  
 20 25 30  
 Leu Ala Arg Ser Gln Ile His Ser Ile Arg Asp Leu Gln Arg Leu Leu  
 35 40 45  
 Glu Ile Asp Ser Val Gly Ser Glu Asp Ser Leu Asp Thr Ser Leu Arg  
 50 55 60  
 Ala His Gly Val His Ala Thr Lys His Val Pro Glu Lys Arg Pro Leu  
 65 70 75 80  
 Pro Ile Arg Arg Lys Arg Ser Ile Glu Glu Ala Val Pro Ala Val Cys  
 85 90 95  
 Lys Thr Arg Thr Val Ile Tyr Glu Ile Pro Arg Ser Gln Val Asp Pro  
 100 105 110  
 Thr Ser Ala Asn Phe Leu Ile Trp Pro Pro Cys Val Glu Val Lys Arg  
 115 120 125  
 Cys Thr Gly Cys Cys Asn Thr Ser Ser Val Lys Cys Gln Pro Ser Arg  
 130 135 140  
 Val His His Arg Ser Val Lys Val Ala Lys Val Glu Tyr Val Arg Lys  
 145 150 155 160  
 Lys Pro Lys Leu Lys Glu Val Gln Val Arg Leu Glu Glu His Leu Glu  
 165 170 175  
 Cys Ala Cys Ala Thr Thr Ser Leu Asn Pro Asp Tyr Arg Glu Glu Asp

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190

Met	Asn	Arg	Cys	Trp	Ala	Leu	Phe	Leu	Ser	Leu	Cys	Cys	Tyr	Leu	Arg
1				5					10					15	
Leu	Val	Ser	Ala	Glu	Gly	Asp	Pro	Ile	Pro	Glu	Glu	Leu	Tyr	Glu	Met
			20					25					30		
Leu	Ser	Asp	His	Ser	Ile	Arg	Ser	Phe	Asp	Asp	Leu	Gln	Arg	Leu	Leu
		35					40					45			
His	Gly	Asp	Pro	Gly	Glu	Glu	Asp	Gly	Ala	Glu	Leu	Asp	Leu	Asn	Met
	50					55					60				
Thr	Arg	Ser	His	Ser	Gly	Gly	Glu	Leu	Glu	Ser	Leu	Ala	Arg	Gly	Arg
65					70					75					80
Arg	Ser	Leu	Gly	Ser	Leu	Thr	Ile	Ala	Glu	Pro	Ala	Met	Ile	Ala	Glu
				85					90					95	
Cys	Lys	Thr	Arg	Thr	Glu	Val	Phe	Glu	Ile	Ser	Arg	Arg	Leu	Ile	Asp
			100					105					110		
Arg	Thr	Asn	Ala	Asn	Phe	Leu	Val	Trp	Pro	Pro	Cys	Val	Glu	Val	Gln
		115					120					125			
Arg	Cys	Ser	Gly	Cys	Cys	Asn	Asn	Arg	Asn	Val	Gln	Cys	Arg	Pro	Thr
	130					135					140				
Gln	Val	Gln	Leu	Arg	Pro	Val	Gln	Val	Arg	Lys	Ile	Glu	Ile	Val	Arg
145					150					155					160
Lys	Lys	Pro	Ile	Phe	Lys	Lys	Ala	Thr	Val	Thr	Leu	Glu	Asp	His	Leu
				165					170					175	
Ala	Cys	Lys	Cys	Glu	Thr	Val	Ala	Ala	Ala	Arg	Pro	Val	Thr	Arg	Ser
			180					185					190		
Pro	Gly	Gly	Ser	Gln	Glu	Gln	Arg	Ala	Lys	Thr	Pro	Gln	Thr	Arg	Val

195	200	205
Thr Ile Arg Thr Val Arg Val Arg Arg Pro Pro Lys Gly Lys His Arg		
210	215	220
Lys Phe Lys His Thr His Asp Lys Thr Ala Leu Lys Glu Thr Leu Gly		
225	230	240
Ala		

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 232 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu		
1	5	10 15
Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly		
	20	25 30
Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln		
	35	40 45
Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu		
	50	55 60
Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu		
	65	70 75 80
Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro		
	85	90 95
Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His		
	100	105 110
Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys		
	115	120 125
Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Lys Ser Val		
	130	135 140
Arg Gly Lys Gly Lys Gly Gln Lys Arg Lys Arg Lys Lys Ser Arg Tyr		
	145	150 155 160
Lys Ser Trp Ser Val Tyr Val Gly Ala Arg Cys Cys Leu Met Pro Trp		

009526 0840  
T04280 9225660

(2) INFORMATION FOR SEQ ID NO:8:

(A) LENGTH: 14 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: not relevant

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

(2) INFORMATION FOR SEO ID NO:9:

(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

18

(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGGTTTTTCCC AGTCACGAC

18

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CCACATGGTT CAGGAAAGAC A

21

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TGTAATACGA CTCACTATAG GGATCCCGCC ATGGAGGCCA CGGCTTATGC

50

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GATCTCTAGA TTAGCTCATT TGTGGTCT

28

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs

099376-02440  
T04280" 92/5E60

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CGCGGATCCA TGACTGTACT CTACCCA

27

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 60 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CGCTCTAGAT CAAGCGTAGT CTGGGACGTC GTATGGGTAC TCGAGGCTCA TTTGTGGTCT

60

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3974 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGTACCTAAG TGAGTAGGGC GTCCGATCGA CGGACGCCTT TTTTTTGAAT TCGTAATCAT	60
GGTCATAGCT GTTTCCTGTG TGAAATTGTT ATCCGCTCAC AATTCACAC AACATACGAG	120
CCGGAAGCAT AAAGTGTAAG GCCTGGGGTG CCTAATGAGT GAGCTAACTC ACATTAATTG	180
CGTTGCGCTC ACTGCCCGCT TTCCAGTCGG GAAACCTGTC GTGCCAGCTG CATTAATGAA	240
TCGGCCAACG CGCGGGGAGA GCGGTTTTGC GTATTGGGCG CTCTTCCGCT TCCTCGCTCA	300
CTGACTCGCT GCGCTCGGTC GTTCGGCTGC GGCGAGCGGT ATCAGCTCAC TCAAAGGCGG	360
TAATACGGTT ATCCACAGAA TCAGGGGATA ACGCAGGAAA GAACATGTGA GCAAAAGGCC	420
AGCAAAAGGC CAGGAACCGT AAAAAGGCCG CGTTGCTGGC GTTTTTCAT AGGCTCCGCC	480

CCCCTGACGA GCATCACAAA AATCGACGCT CAAGTCAGAG GTGGCGAAAC CCGACAGGAC	540
TATAAAGATA CCAGGCGTTT CCCCCTGGAA GCTCCCTCGT GCGCTCTCCT GTTCCGACCC	600
TGCCGCTTAC CGGATACCTG TCCGCCTTTC TCCCTTCGGG AAGCGTGGCG CTTTCTCATA	660
GCTCACGCTG TAGGTATCTC AGTTCGGTGT AGGTCGTTCT CTCCAAGCTG GGCTGTGTGC	720
ACGAACCCCC CGTTCAGCCC GACCGCTGCG CTTTATCCGG TAACTATCGT CTTGAGTCCA	780
ACCCGGTAAG ACACGACTTA TCGCCACTGG CAGCAGCCAC TGATAACAGG ATTAGCAGAG	840
CGAGGTATGT AGGCGGTGCT ACAGAGTTCT TGAAGTGGTG GCCTAACTAC GGCTACACTA	900
GAAGAACAGT ATTTGGTATC TCGCTCTGC TGAAGCCAGT TACCTTCGGA AAAAGAGTTG	960
GTAGCTCTTG ATCCGGCAAA CAAACCACCG CTGGTAGCGG TGGTTTTTTT GTTTGCAAGC	1020
AGCAGATTAC GCGCAGAAAA AAAGGATCTC AAGAAGATCC TTTGATCTTT TCTACGGGGT	1080
CTGACGCTCA GTGGAACGAA AACTCACGTT AAGGGATTTT GGTCAATGAGA TTATCGTCGA	1140
CAATTCGCGC GCGAAGGCGA AGCGGCATGC ATTTACGTTG ACACCATCGA ATGGTGCAAA	1200
ACCTTTTCGG GTATGGCATG ATAGCGCCCG GAAGAGAGTC AATTCAGGGT GGTGAATGTG	1260
AAACCAGTAA CGTTATACGA TGTCGCAGAG TATGCCGGTG TCTCTTATCA GACCGTTTCC	1320
CGCGTGGTGA ACCAGGCCAG CCACGTTTCT GCGAAAACGC GGGAAAAAGT GGAAGCGGCG	1380
ATGGCGGAGC TGAATTACAT TCCCAACCGC GTGGCACAAC AACTGGCGGG CAAACAGTCG	1440
TTGCTGATTG GCGTTGCCAC CTCCAGTCTG GCCCTGCACG CGCCGTCGCA AATTGTGCGG	1500
GCGATTAAAT CTCGCGCCGA TCAACTGGGT GCCAGCGTGG TGGTGTGAT GGTAGAACGA	1560
AGCGGCGTCG AAGCCTGTAA AGCGGCGGTG CACAATCTTC TCGCGCAACG CGTCAGTGGG	1620
CTGATCATTA ACTATCCGCT GGATGACCAG GATGCCATTG CTGTGGAAGC TGCCTGCACT	1680
AATGTTCCGG CGTTATTCTT TGATGTCTCT GACCAGACAC CCATCAACAG TATTATTTTC	1740
TCCCATGAAG ACGGTACGCG ACTGGGCGTG GAGCATCTGG TCGCATTGGG TCACCAGCAA	1800
ATCGCGCTGT TAGCGGGCCC ATTAAGTTCT GTCTCGGCGC GTCTGCGTCT GGCTGGCTGG	1860
CATAAATATC TCACTCGCAA TCAAATTCAG CCGATAGCGG AACGGGAAGG CGACTGGAGT	1920
GCCATGTCCG GTTTTCAACA AACCATGCAA ATGCTGAATG AGGGCATCGT TCCCACTGCG	1980
ATGCTGGTTG CCAACGATCA GATGGCGCTG GCGCAATGC GCGCCATTAC CGAGTCCGGG	2040
CTGCGCGTTG GTGCGGATAT CTCGGTAGTG GGATACGACG ATACCGAAGA CAGCTCATGT	2100
TATATCCCGC CGTTAACCAC CATCAAACAG GATTTTCGCC TGCTGGGGCA AACCAGCGTG	2160

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GACCGCTTGC TGCAACTCTC TCAGGGCCAG GCGGTGAAGG GCAATCAGCT GTTGCCCCGTC	2220
TCACTGGTGA AAAGAAAAAC CACCCTGGCG CCCAATACGC AAACCGCCTC TCCCCGCGCG	2280
TTGGCCGATT CATTAATGCA GCTGGCACGA CAGGTTTCCC GACTGGAAAG CGGGCAGTGA	2340
GCGCAACGCA ATTAATGTAA GTTAGCGCGA ATTGTCGACC AAAGCGGCCA TCGTGCCTCC	2400
CCACTCCTGC AGTTCGGGGG CATGGATGCG CGGATAGCCG CTGCTGGTTT CCTGGATGCC	2460
GACGGATTTG CACTGCCGGT AGAACTCCGC GAGGTCGTCC AGCCTCAGGC AGCAGCTGAA	2520
CCAACTCGCG AGGGGATCGA GCCCAGGGTG GGCGAAGAAC TCCAGCATGA GATCCCCGCG	2580
CTGGAGGATC ATCCAGCCGG CGTCCCGGAA AACGATTCCG AAGCCCAACC TTTCATAGAA	2640
GGCGGCGGTG GAATCGAAAT CTCGTGATGG CAGGTTGGGC GTCGCTTGGT CCGTCATTTT	2700
GAACCCCAAG GTCCCGCTCA GAAGAACTCG TCAAGAAGGC GATAGAAGGC GATGCGCTGC	2760
GAATCGGGAG CGGCGATACC GTAAAGCACG AGGAAGCGGT CAGCCCATTC GCCGCAAGC	2820
TCTTCAGCAA TATCACGGGT AGCCAACGCT ATGTCCTGAT AGCGGTCCGC CACACCCAGC	2880
CGGCCACAGT CGATGAATCC AGAAAAGCGG CCATTTTCCA CCATGATATT CGGCAAGCAG	2940
GCATCGCCAT GGGTCACGAC GAGATCCTCG CCGTCGGGCA TGC CGCCTT GAGCCTGGCG	3000
AACAGTTCGG CTGGCGCGAG CCCCTGATGC TCTTCGTCCA GATCATCCTG ATCGACAAGA	3060
CCGGCTTCCA TCCGAGTACG TGCTCGCTCG ATGCGATGTT TCGCTTGGTG GTCGAATGGG	3120
CAGGTAGCCG GATCAAGCGT ATGCAGCCGC CGCATTGCAT CAGCCATGAT GGATACTTTC	3180
TCGGCAGGAG CAAGGTGAGA TGACAGGAGA TCCTGCCCCG GCACTTCGCC CAATAGCAGC	3240
CAGTCCCTTC CCGCTTCAGT GACAACGTCG AGCACAGCTG CGCAAGGAAC GCCCGTCGTG	3300
GCCAGCCACG ATAGCCGCGC TGCCTCGTCC TGCAGTTCAT TCAGGGCACC GGACAGGTG	3360
GTCTTGACAA AAAGAACCGG GCGCCCCCTGC GCTGACAGCC GGAACACGGC GGCATCAGAG	3420
CAGCCGATTG TCTGTTGTGC CCAGTCATAG CCGAATAGCC TCTCCACCCA AGCGGCCGGA	3480
GAACCTGCGT GCAATCCATC TTGTTCAATC ATGCGAAACG ATCCTCATCC TGTCTCTTGA	3540
TCAGATCTTG ATCCCCTGCG CCATCAGATC CTTGGCGGCA AGAAAGCCAT CCAGTTTACT	3600
TTGCAGGGCT TCCCAACCTT ACCAGAGGGC GCCCCAGCTG GCAATTCCGG TTCGCTTGCT	3660
GTCCATAAAA CCGCCAGTC TAGCTATCGC CATGTAAGCC CACTGCAAGC TACCTGCTTT	3720
CTCTTTGCGC TTGCGTTTTT CCTTGTCCAG ATAGCCAGT AGCTGACATT CATCCGGGGT	3780
CAGCACCGTT TCTGCGGACT GGCTTTCTAC GTGTTCCGCT TCCTTTAGCA GCCCTTGCGC	3840

CCTGAGTGTCT TCGGGCAGCG TGAAGCTTAA AAAACTGCAA AAAATAGTTT GACTTGTGAG 3900  
 CGGATAACAA TTAAGATGTA CCAATTGTG AGCGGATAAC AATTCACAC ATTAAAGAGG 3960  
 AGAAATTACA TATG 3974

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 112 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

AAGCTTAAAA AACTGCAAAA AATAGTTTGA CTTGTGAGCG GATAACAATT AAGATGTACC 60  
 CAATTGTGAG CGGATAACAA TTTCACACAT TAAAGAGGAG AAATTACATA TG 112

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 419 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met His Ser Leu Gly Phe Phe Ser Val Ala Cys Ser Leu Leu Ala Ala  
 1 5 10 15  
 Ala Leu Leu Pro Gly Pro Arg Glu Ala Pro Ala Ala Ala Ala Phe  
 20 25 30  
 Glu Ser Gly Leu Asp Leu Ser Asp Ala Glu Pro Asp Ala Gly Glu Ala  
 35 40 45  
 Thr Ala Tyr Ala Ser Lys Asp Leu Glu Glu Gln Leu Arg Ser Val Ser  
 50 55 60  
 Ser Val Asp Glu Leu Met Thr Val Leu Tyr Pro Glu Tyr Trp Lys Met  
 65 70 75 80  
 Tyr Lys Cys Gln Leu Arg Lys Gly Gly Trp Gln His Asn Arg Glu Gln  
 85 90 95

009426-0240

Ala Asn Leu Asn Ser Arg Thr Glu Glu Thr Ile Lys Phe Ala Ala Ala  
100 105 110

His Tyr Asn Thr Glu Ile Leu Lys Ser Ile Asp Asn Glu Trp Arg Lys  
115 120 125

Thr Gln Cys Met Pro Arg Glu Val Cys Ile Asp Val Gly Lys Glu Phe  
130 135 140

Gly Val Ala Thr Asn Thr Phe Phe Lys Pro Pro Cys Val Ser Val Tyr  
145 150 155 160

Arg Cys Gly Gly Cys Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Thr  
165 170 175

Ser Thr Ser Tyr Leu Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu  
180 185 190

Ser Gln Gly Pro Lys Pro Val Thr Ile Ser Phe Ala Asn His Thr Ser  
195 200 205

Cys Arg Cys Met Ser Lys Leu Asp Val Tyr Arg Gln Val His Ser Ile  
210 215 220

Ile Arg Arg Ser Leu Pro Ala Thr Leu Pro Gln Cys Gln Ala Ala Asn  
225 230 235 240

Lys Thr Cys Pro Thr Asn Tyr Met Trp Asn Asn His Ile Cys Arg Cys  
245 250 255

Leu Ala Gln Glu Asp Phe Met Phe Ser Ser Asp Ala Gly Asp Asp Ser  
260 265 270

Thr Asp Gly Phe His Asp Ile Cys Gly Pro Asn Lys Glu Leu Asp Glu  
275 280 285

Glu Thr Cys Gln Cys Val Cys Arg Ala Gly Leu Arg Pro Ala Ser Cys  
290 295 300

Gly Pro His Lys Glu Leu Asp Arg Asn Ser Cys Gln Cys Val Cys Lys  
305 310 315 320

Asn Lys Leu Phe Pro Ser Gln Cys Gly Ala Asn Arg Glu Phe Asp Glu  
325 330 335

Asn Thr Cys Gln Cys Val Cys Lys Arg Thr Cys Pro Arg Asn Gln Pro  
340 345 350

Leu Asn Pro Gly Lys Cys Ala Cys Glu Cys Thr Glu Ser Pro Gln Lys  
355 360 365

Cys Leu Leu Lys Gly Lys Lys Phe His His Gln Thr Cys Ser Cys Tyr  
370 375 380

Arg Arg Pro Cys Thr Asn Arg Gln Lys Ala Cys Glu Pro Gly Phe Ser

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385		390		395		400									
Tyr	Ser	Glu	Glu	Val	Cys	Arg	Cys	Val	Pro	Ser	Tyr	Trp	Gln	Arg	Pro
				405					410					415	
Gln Met Ser															

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GCAGCACATA TGACAGAAGA GACTATAAAA 30

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GCAGCAGGTA CCTCACAGTT TAGACATGCA 30

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GCAGCAGGTA CCTCAACGTC TAATAATGGA 30

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GCAGCAGGAT CCCACAGAAG AGACTATAAA

30

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GCAGCATCTA GATCACAGTT TAGACATGCA

30

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GCAGCAGGAT CCCACAGAAG AGACTATAAA ATTTGCTGC

39

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

00422200 92/03/65

GCAGCATCTA GATCAACGTC TAATAATGGA ATGAAC

36

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 55 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GATCGATCCA TCATGCACTC GCTGGGCTTC TTCTCTGTGG CGTGTCTCTCT GCTCG

55

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GCAGGGTACG GATCCTAGAT TAGCTCATTT GTGGTCTTT

39

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GACTGGATCC GCCACCATGC ACTCGCTGGG CTTCTTCTC

39

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GACTGGTACC TTATCACATA AAATCTTCCT GAGCC

35

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GACTGGATCC GCCACCATGC ACTCGCTGGG CTTCTTCTC

39

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GACTGGTACC TTATCAGTCT AGTTCTTTGT GGGG

34

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GACTGGATCC GCCACCATGC ACTCGCTGGG CTTCTTCTC

39

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

093376-082401  
T04280"92456560

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GACTGGTACC TCATTACTGT GGACTTTCTG TACATTC

37

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GCAGCAGGAT CCACAGAAGA GACTATAAAA TTTGCTGC

38

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

CGTCGTTCTA GATCACAGT TAGACATGCA TCGGCAG

37

003572 0840  
"9245660"